

SEQUENCE LISTING

(1) GENERAL INFORMATION:

- (i) APPLICANT: De Robertis, Edward M.
Bouwmeester, Tewis
- (ii) TITLE OF INVENTION: Endoderm, Cardiac and Neural Inducing
Factors
- (iii) NUMBER OF SEQUENCES: 10
- (iv) CORRESPONDENCE ADDRESS:
 - (A) ADDRESSEE: Majestic, Parsons, Siebert & Hsue
 - (B) STREET: Four Embarcadero Center, Suite 1100
 - (C) CITY: San Francisco
 - (D) STATE: California
 - (E) COUNTRY: U.S.A.
 - (F) ZIP: 94111-4106
- (v) COMPUTER READABLE FORM:
 - (A) MEDIUM TYPE: Floppy disk
 - (B) COMPUTER: IBM PC compatible
 - (C) OPERATING SYSTEM: PC-DOS/MS-DOS
 - (D) SOFTWARE: PatentIn Release #1.0, Version #1.25
- (vi) CURRENT APPLICATION DATA:
 - (A) APPLICATION NUMBER: US 08/878,474
 - (B) FILING DATE: 18-JUN-1997
 - (C) CLASSIFICATION:
- (vii) PRIOR APPLICATION DATA:
 - (A) APPLICATION NUMBER: US 60/020,150
 - (B) FILING DATE: 20-JUN-1996
- (viii) ATTORNEY/AGENT INFORMATION:
 - (A) NAME: Siebert, J. Suzanne
 - (B) REGISTRATION NUMBER: 28,758
 - (C) REFERENCE/DOCKET NUMBER: 3100.002US1
- (ix) TELECOMMUNICATION INFORMATION:
 - (A) TELEPHONE: 415/248-5500
 - (B) TELEFAX: 415/362-5418

(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 270 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

Met Leu Leu Asn Val Leu Arg Ile Cys Ile Ile Val Cys Leu Val Asn
1 5 10 15
Asp Gly Ala Gly Lys His Ser Glu Gly Arg Glu Arg Thr Lys Thr Tyr
20 25 30
Ser Leu Asn Ser Arg Gly Tyr Phe Arg Lys Glu Arg Gly Ala Arg Arg
35 40 45
Ser Lys Ile Leu Leu Val Asn Thr Lys Gly Leu Asp Glu Pro His Ile
50 55 60
Gly His Gly Asp Phe Gly Leu Val Ala Glu Leu Phe Asp Ser Thr Arg
65 70 75 80
Thr His Thr Asn Arg Lys Glu Pro Asp Met Asn Lys Val Lys Leu Phe
85 90 95
Ser Thr Val Ala His Gly Asn Lys Ser Ala Arg Arg Lys Ala Tyr Asn
100 105 110
Gly Ser Arg Arg Asn Ile Phe Ser Arg Arg Ser Phe Asp Lys Arg Asn
115 120 125
Thr Glu Val Thr Glu Lys Pro Gly Ala Lys Met Phe Trp Asn Asn Phe
130 135 140
Leu Val Lys Met Asn Gly Ala Pro Gln Asn Thr Ser His Gly Ser Lys
145 150 155 160
Ala Gln Glu Ile Met Lys Glu Ala Cys Lys Thr Leu Pro Phe Thr Gln
165 170 175
Asn Ile Val His Glu Asn Cys Asp Arg Met Val Ile Gln Asn Asn Leu
180 185 190
Cys Phe Gly Lys Cys Ile Ser Leu His Val Pro Asn Gln Gln Asp Arg
195 200 205
Arg Asn Thr Cys Ser His Cys Leu Pro Ser Lys Phe Thr Leu Asn His
210 215 220

Leu Thr Leu Asn Cys Thr Gly Ser Lys Asn Val Val Lys Val Val Met
 225 230 235 240

Met Val Glu Glu Cys Thr Cys Glu Ala His Lys Ser Asn Phe His Gln
 245 250 255

Thr Ala Gln Phe Asn Met Asp Thr Ser Thr Thr Leu His His
 260 265 270

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1411 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

GAATTCCTAA AAGCGGCACA GTGCAGGAAC AGCAAGTCGC TCAGAAACAC TGCAGGGTCT	60
AGATATCATA CAATGTTACT AAATGTACTC AGGATCTGTA TTATCGTCTG CCTTGTGAAT	120
GATGGAGCAG GAAACACTC AGAAGGACGA GAAAGGACAA AAACATATTC ACTTAACAGC	180
AGAGGTTACT TCAGAAAAGA AAGAGGAGCA CGTAGGAGCA AGATTCTGCT GGTGAATACT	240
AAAGGTCTTG ATGAACCCCA CATTGGGCAT GGTGATTTTG GCTTAGTAGC TGAACTATTT	300
GATTCCACCA GAACACATAC AAACAGAAAA GAGCCAGACA TGAACAAAGT CAAGCTTTTC	360
TCAACAGTTG CCCATGGAAA CAAAAGTGCA AGAAGAAAAG CTTACAATGG TTCTAGAAGG	420
AATATTTTTT CTCGCCGTTT TTTTGATAAA AGAAATACAG AGGTTACTGA AAAGCCTGGT	480
GCCAAGATGT TCTGGAACAA TTTTTTGGTT AAAATGAATG GAGCCCCACA GAATACAAGC	540
CATGGCAGTA AAGCACAGGA AATAATGAAA GAAGCTTGCA AAACCTTGCC CTTCACTCAG	600
AATATTGTAC ATGAAACTG TGACAGGATG GTGATACAGA ACAATCTGTG CTTTGGTAAA	660
TGCATCTCTC TCCATGTTCC AAATCAGCAA GATCGACGAA ATACTTGTTT CCATTGCTTG	720
CCGTCCAAAT TTACCCTGAA CCACCTGACG CTGAATTGTA CTGGATCTAA GAATGTAGTA	780
AAGGTTGTCA TGATGGTAGA GGAATGCACG TGTGAAGCTC ATAAGAGCAA CTTCCACCAA	840

ACTGCACAGT TTAACATGGA TACATCTACT ACCCTGCACC ATTAAAAGGA CTGTCTGCCA 900
TACAGTATGG AAATGCCCAT TTGTTGGAAT ATTCGTTACA TGCTATGTAT CTAAAGCATT 960
ATGTTGCCTT CTGTTTCATA TAACCACATG GAATAAGGAT TGTATGAATT ATAATTAACA 1020
AATGGCATT TGTGTAACAT GCAAGATCTC TGTTCATCA GTTGCAAGAT AAAAGGCAAT 1080
ATTTGTTTGA CTTTTTCTA CAAAATGAAT ACCCAAATAT ATGATAAGAT AATGGGGTCA 1140
AAACTGTTAA GGGGTAATGT AATAATAGGG ACTAACAACC AATCAGCAGG TATGATTTAC 1200
TGGTCACCTG TTTAAAAGCA AACATCTTAT TGGTTGCTAT GGGTTACTGC TTCTGGGCAA 1260
AATGTGTGCC TCATAGGGGG GTTAGTGTGT TGTGTACTGA ATTAATTGTA TTTATTTTAT 1320
TGTTACAATG AAGAGGATGT CTATGTTTAT TTCACTTTTA TTAATGTACA ATAAATGTTC 1380
TTGTTTCTTT AAAAAAAAAA AAAAATCTGA G 1411

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 318 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

Met Ser Arg Thr Arg Lys Val Asp Ser Leu Leu Leu Leu Ala Ile Pro
1 5 10 15
Gly Leu Ala Leu Leu Leu Leu Pro Asn Ala Tyr Cys Ala Ser Cys Glu
20 25 30
Pro Val Arg Ile Pro Met Cys Lys Ser Met Pro Trp Asn Met Thr Lys
35 40 45
Met Pro Asn His Leu His His Ser Thr Gln Ala Asn Ala Ile Leu Ala
50 55 60
Ile Glu Gln Phe Glu Gly Leu Leu Thr Thr Glu Cys Ser Gln Asp Leu
65 70 75 80
Leu Phe Phe Leu Cys Ala Met Tyr Ala Pro Ile Cys Thr Ile Asp Phe
85 90 95

Gln His Glu Pro Ile Lys Pro Cys Lys Ser Val Cys Glu Arg Ala Arg
 100 105 110
 Ala Gly Cys Glu Pro Ile Leu Ile Lys Tyr Arg His Thr Trp Pro Glu
 115 120 125
 Ser Leu Ala Cys Glu Glu Leu Pro Val Tyr Asp Arg Gly Val Cys Ile
 130 135 140
 Ser Pro Glu Ala Ile Val Thr Val Glu Gln Gly Thr Asp Ser Met Pro
 145 150 155 160
 Asp Phe Ser Met Asp Ser Asn Asn Gly Asn Cys Gly Ser Gly Arg Glu
 165 170 175
 His Cys Lys Cys Lys Pro Met Lys Ala Thr Gln Lys Thr Tyr Leu Lys
 180 185 190
 Asn Asn Tyr Asn Tyr Val Ile Arg Ala Lys Val Lys Glu Val Lys Val
 195 200 205
 Lys Cys His Asp Ala Thr Ala Ile Val Glu Val Lys Glu Ile Leu Lys
 210 215 220
 Ser Ser Leu Val Asn Ile Pro Lys Asp Thr Val Thr Leu Tyr Thr Asn
 225 230 235 240
 Ser Gly Cys Leu Cys Pro Gln Leu Val Ala Asn Glu Glu Tyr Ile Ile
 245 250 255
 Met Gly Tyr Glu Asp Lys Glu Arg Thr Arg Leu Leu Leu Val Glu Gly
 260 265 270
 Ser Leu Ala Glu Lys Trp Arg Asp Arg Leu Ala Lys Lys Val Lys Arg
 275 280 285
 Trp Asp Gln Lys Leu Arg Arg Pro Arg Lys Ser Lys Asp Pro Val Ala
 290 295 300
 Pro Ile Pro Asn Lys Asn Ser Asn Ser Arg Gln Ala Arg Ser
 305 310 315

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1875 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

GAATTCCTT TCACACAGGA CTCCTGGCAG AGGTGAATGG TTAGCCCTAT GGATTGGTT 60
TGTTGATTTT GACACATGAT TGATTGCTTT CAGATAGGAT TGAAGGACTT GGATTTTAT 120
CTAATTCTGC ACTTTTAAAT TATCTGAGTA ATTGTTTATT TTGTATTGGA TGGGACTAAA 180
GATAAACTTA ACTCCTTGCT TTTGACTTGC CCATAAACTA TAAGGTGGGG TGAGTTGTAG 240
TTGCTTTTAC ATGTGCCCAG ATTTTCCCTG TATTCCTGT ATTCCCTCTA AAGTAAGCCT 300
ACACATACAG GTTGGGCAGA ATAACAATGT CTCGAACAAG GAAAGTGGAC TCATTACTGC 360
TACTGGCCAT ACCTGGACTG GCGCTTCTCT TATTACCCAA TGCTTACTGT GCTTCGTGTG 420
AGCCTGTGCG GATCCCCATG TGCAAATCTA TGCCATGGAA CATGACCAAG ATGCCCAACC 480
ATCTCCACCA CAGCACTCAA GCCAATGCCA TCCTGGCAAT TGAACAGTTT GAAGGTTTGC 540
TGACCACTGA ATGTAGCCAG GACCTTTTGT TCTTTCTGTG TGCCATGTAT GCCCCATTT 600
GTACCATCGA TTTCCAGCAT GAACCAATTA AGCCTTGCAA GTCCGTGTGC GAAAGGGCCA 660
GGGCCGGCTG TGAGCCCATT CTCATAAAGT ACCGGCACAC TTGGCCAGAG AGCCTGGCAT 720
GTGAAGAGCT GCCCGTATAT GACAGAGGAG TCTGCATCTC CCCAGAGGCT ATCGTCACAG 780
TGGAACAAGG AACAGATTCA ATGCCAGACT TCTCCATGGA TTCAAACAAT GGAAATTGCG 840
GAAGCGGCAG GGAGCACTGT AAATGCAAGC CCATGAAGGC AACCCAAAAG ACGTATCTCA 900
AGAATAATTA CAATTATGTA ATCAGAGCAA AAGTGAAAGA GGTGAAAGTG AAATGCCACG 960
ACGCAACAGC AATTGTGGAA GTAAAGGAGA TTCTCAAGTC TTCCCTAGTG AACATTCCTA 1020
AAGACACAGT GACACTGTAC ACCAACTCAG GCTGCTTGTG CCCCCAGCTT GTTGCCAATG 1080
AGGAATACAT AATTATGGGC TATGAAGACA AAGAGCGTAC CAGGCTTCTA CTAGTGGGAAG 1140
GATCCTTGGC CGAAAAATGG AGAGATCGTC TTGCTAAGAA AGTCAAGCGC TGGGATCAAA 1200
AGCTTCGACG TCCCAGGAAA AGCAAAGACC CCGTGGCTCC AATTCCCAAC AAAAACAGCA 1260
ATTCCAGACA AGCGCGTAGT TAGACTAACG GAAAGGTGTA TGGAAGTCT ATGGACTTTG 1320
AAACTAAGAT TTGCATTGTT GGAAGAGCAA AAAAGAAATT GCACTACAGC ACGTTATATT 1380
CTATTGTTTA CTACAAGAAG CTGGTTTAGT TGATTGTAGT TCTCCTTTCC TTCTTTTTTT 1440

TTATAACTAT ATTTGCACGT GTTCCCAGGC AATTGTTTTA TTCAACTTCC AGTGACAGAG 1500
 CAGTGACTGA ATGTCTCAGC CTAAAGAAGC TCAATTCATT TCTGATCAAC TAATGGTGAC 1560
 AAGTGTTTGA TACTTGGGGA AAGTGAAC TAATTGCAATGG TAAATCAGAG AAAAGTTGAC 1620
 CAATGTTGCT TTTCTGTAG ATGAACAAGT GAGAGATCAC ATTTAAATGA TGATCACTTT 1680
 CCATTTAATA CTTTCAGCAG TTTTAGTTAG ATGACATGTA GGATGCACCT AAATCTAAAT 1740
 ATTTTATCAT AAATGAAGAG CTGGTTTAGA CTGTATGGTC ACTGTTGGGA AGGTAAATGC 1800
 CTACTTTGTC AATTCTGTTT TAAAAATTGC CTAAATAAAT ATTAAGTCCT AAATAAAAAA 1860
 AAAAAAAAAA AAAAA 1875

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 979 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

Met Leu Leu Leu Phe Arg Ala Ile Pro Met Leu Leu Leu Gly Leu Met
 1 5 10 15
 Val Leu Gln Thr Asp Cys Glu Ile Ala Gln Tyr Tyr Ile Asp Glu Glu
 20 25 30
 Glu Pro Pro Gly Thr Val Ile Ala Val Leu Ser Gln His Ser Ile Phe
 35 40 45
 Asn Thr Thr Asp Ile Pro Ala Thr Asn Phe Arg Leu Met Lys Gln Phe
 50 55 60
 Asn Asn Ser Leu Ile Gly Val Arg Glu Ser Asp Gly Gln Leu Ser Ile
 65 70 75 80
 Met Glu Arg Ile Asp Arg Glu Gln Ile Cys Arg Gln Ser Leu His Cys
 85 90 95
 Asn Leu Ala Leu Asp Val Val Ser Phe Ser Lys Gly His Phe Lys Leu
 100 105 110

Gly Gln Val Arg Cys Thr Leu Tyr Gly His Glu His Phe Lys Leu Gln
 385 390 395 400
 Gln Ala Tyr Glu Asp Ser Tyr Met Ile Val Thr Thr Ser Thr Leu Asp
 405 410 415
 Arg Glu Asn Ile Ala Ala Tyr Ser Leu Thr Val Val Ala Glu Asp Leu
 420 425 430
 Gly Phe Pro Ser Leu Lys Thr Lys Lys Tyr Tyr Thr Val Lys Val Ser
 435 440 445
 Asp Glu Asn Asp Asn Ala Pro Val Phe Ser Lys Pro Gln Tyr Glu Ala
 450 455 460
 Ser Ile Leu Glu Asn Asn Ala Pro Gly Ser Tyr Ile Thr Thr Val Ile
 465 470 475 480
 Ala Arg Asp Ser Asp Ser Asp Gln Asn Gly Lys Val Asn Tyr Arg Leu
 485 490 495
 Val Asp Ala Lys Val Met Gly Gln Ser Leu Thr Thr Phe Val Ser Leu
 500 505 510
 Asp Ala Asp Ser Gly Val Leu Arg Ala Val Arg Ser Leu Asp Tyr Glu
 515 520 525
 Lys Leu Lys Gln Leu Asp Phe Glu Ile Glu Ala Ala Asp Asn Gly Ile
 530 535 540
 Pro Gln Leu Ser Thr Arg Val Gln Leu Asn Leu Arg Ile Val Asp Gln
 545 550 555 560
 Asn Asp Asn Cys Pro Val Ile Thr Asn Pro Leu Leu Asn Asn Gly Ser
 565 570 575
 Gly Glu Val Leu Leu Pro Ile Ser Ala Pro Gln Asn Tyr Leu Val Phe
 580 585 590
 Gln Leu Lys Ala Glu Asp Ser Asp Glu Gly His Asn Ser Gln Leu Phe
 595 600 605
 Tyr Thr Ile Leu Arg Asp Pro Ser Arg Leu Phe Ala Ile Asn Lys Glu
 610 615 620
 Ser Gly Glu Val Phe Leu Lys Lys Gln Leu Asn Ser Asp His Ser Glu
 625 630 635 640
 Asp Leu Ser Ile Val Val Ala Val Tyr Asp Leu Gly Arg Pro Ser Leu
 645 650 655

Ser Thr Asn Ala Thr Val Lys Phe Ile Leu Thr Asp Ser Phe Pro Ser
660 665 670

Asn Val Glu Val Val Ile Leu Gln Pro Ser Ala Glu Glu Gln His Gln
675 680 685

Ile Asp Met Ser Ile Ile Phe Ile Ala Val Leu Ala Gly Gly Cys Ala
690 695 700

Leu Leu Leu Leu Ala Ile Phe Phe Val Ala Cys Thr Cys Lys Lys Lys
705 710 715 720

Ala Gly Glu Phe Lys Gln Val Pro Glu Gln His Gly Thr Cys Asn Glu
725 730 735

Glu Arg Leu Leu Ser Thr Pro Ser Pro Gln Ser Val Ser Ser Ser Leu
740 745 750

Ser Gln Ser Glu Ser Cys Gln Leu Ser Ile Asn Thr Glu Ser Glu Asn
755 760 765

Cys Ser Val Ser Ser Asn Gln Glu Gln His Gln Gln Thr Gly Ile Lys
770 775 780

His Ser Ile Ser Val Pro Ser Tyr His Thr Ser Gly Trp His Leu Asp
785 790 795 800

Asn Cys Ala Met Ser Ile Ser Gly His Ser His Met Gly His Ile Ser
805 810 815

Thr Lys Asp Ser Gly Lys Gly Asp Ser Asp Phe Asn Asp Ser Asp Ser
820 825 830

Asp Thr Ser Gly Glu Ser Gln Lys Lys Ser Ile Glu Gln Pro Met Gln
835 840 845

Ala Gln Ala Ser Ala Gln Tyr Thr Asp Glu Ser Ala Gly Phe Arg His
850 855 860

Ala Asp Asn Tyr Phe Ser His Arg Ile Asn Lys Gly Pro Glu Asn Gly
865 870 875 880

Asn Cys Thr Leu Gln Tyr Glu Lys Gly Tyr Arg Leu Ser Tyr Ser Val
885 890 895

Ala Pro Ala His Tyr Asn Thr Tyr His Ala Arg Met Pro Asn Leu His
900 905 910

Ile Pro Asn His Thr Leu Arg Asp Pro Tyr Tyr His Ile Asn Asn Pro
915 920 925

Val	Ala	Asn	Arg	Met	His	Ala	Glu	Tyr	Glu	Arg	Asp	Leu	Val	Asn	Arg
930						935					940				
Ser	Ala	Thr	Leu	Ser	Pro	Gln	Arg	Ser	Ser	Ser	Arg	Tyr	Gln	Glu	Phe
945					950					955					960
Asn	Tyr	Ser	Pro	Gln	Ile	Ser	Arg	Gln	Leu	His	Pro	Ser	Glu	Ile	Ala
				965					970					975	
Thr	Thr	Phe													

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 3655 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

GAATTC	CCAG	AGATGA	ACTC	CTTGAG	ATTG	TTTTAA	ATGA	CTGCAG	GTCT	GGAAGG	ATTG	60
ACATTG	CCAC	ACTGTT	TCTA	GGCATG	AAAA	AACTGC	AAGT	TTCAAC	TTTG	TTTTTG	GTGC	120
AACTTT	GATT	CTTCAAG	ATG	CTGCTT	CTCT	TCAGAG	CCAT	TCCAAT	GCTG	CTGTTG	GGGAC	180
TGATGG	TTTT	ACAAAC	AGAC	TGTGAA	ATTG	CCCAGT	ACTA	CATAGAT	GAA	GAAGAACC	CCCC	240
CTGGCA	CTGT	AATTGC	AGTG	TTGTCAC	AAC	ACTCCAT	ATT	TAACACT	TACA	GATATAC	CTG	300
CAACCA	ATTT	CCGTCT	AATG	AAGCAAT	TTA	ATAATT	CCCT	TATCGG	AGTC	CGTGAG	AGTG	360
ATGGGC	CAGCT	GAGCAT	CATG	GAGAGG	ATTG	ACCGGG	AGCA	AATCTG	CAGG	CAGTCC	CCTC	420
ACTGCA	ACCT	GGCTTT	GGAT	GTGGTC	AGCT	TTTCCA	AAGG	ACACTT	CAAG	CTTCTG	AACG	480
TGAAAG	TGGA	GGTGAG	AGAC	ATTAAT	GACC	ATAGCC	CCTCA	CTTTCC	CAGT	GAAATA	AATGC	540
ATGTGG	AGGT	GTCTGA	AAGT	TCCTCT	GTGG	GCACCAG	GAT	TCCTTT	AGAA	ATTGCA	ATAG	600
ATGAAG	ATGT	TGGGTCC	AAC	TCCATCC	AGA	ACTTTC	AGAT	CTCAAATA	AAT	AGCCACT	TCA	660
GCATTG	ATGT	GCTAAC	CAGA	GCAGAT	GGGG	TGAAAT	ATGC	AGATTT	AGTC	TTAATG	AGAG	720
AACTGG	ACAG	GGAAAT	CCAG	CCAACAT	ACA	TAATGG	AGCT	ACTAGCA	AATG	GATGGGG	GTG	780

TACCATCACT ATCTGGTACT GCAGTGGTTA ACATCCGAGT CCTGGACTTT AATGATAACA	840
GCCCAGTGTT TGAGAGAAGC ACCATTGCTG TGGACCTAGT AGAGGATGCT CCTCTGGGAT	900
ACCTTTTGTT GGAGTTACAT GCTACTGACG ATGATGAAGG AGTGAATGGA GAAATTGTTT	960
ATGGATTCAG CACTTTGGCA TCTCAAGAGG TACGTCAGCT ATTTAAAATT AACTCCAGAA	1020
CTGGCAGTGT TACTCTTGAA GGCCAAGTTG ATTTTGAGAC CAAGCAGACT TACGAATTTG	1080
AGGTACAAGC CCAAGATTTG GGCCCCAACC CACTGACTGC TACTTGTAAG GTAAGTGTTC	1140
ATATACTTGA TGTAATGAT AATACCCAG CCATCACTAT TACCCCTCTG ACTACTGTAA	1200
ATGCAGGAGT TGCCTATATT CCAGAAACAG CCACAAAGGA GAACTTTATA GCTCTGATCA	1260
GCACTACTGA CAGAGCCTCT GGATCTAATG GACAAGTTCG CTGTACTCTT TATGGACATG	1320
AGCACTTTAA ACTACAGCAA GCTTATGAGG ACAGTTACAT GATAGTTACC ACCTCTACTT	1380
TAGACAGGGA AAACATAGCA GCGTACTCTT TGACAGTAGT TGCAGAAGAC CTTGGCTTCC	1440
CCTCATTGAA GACCAAAAAG TACTACACAG TCAAGGTTAG TGATGAGAAT GACAATGCAC	1500
CTGTATTTTC TAAACCCAG TATGAAGCTT CTATTCTGGA AAATAATGCT CCAGGCTCTT	1560
ATATACTAC AGTGATAGCC AGAGACTCTG ATAGTGATCA AAATGGCAAA GTAAATTACA	1620
GACTTGTGGA TGCAAAAGTG ATGGGCCAGT CACTAACAAC ATTTGTTTCT CTTGATGCGG	1680
ACTCTGGAGT ATTGAGAGCT GTTAGGTCTT TAGACTATGA AAAACTTAAA CAACTGGATT	1740
TTGAAATTGA AGCTGCAGAC AATGGGATCC CTCAACTCTC CACTCGCGTT CAACTAAATC	1800
TCAGAATAGT TGATCAAAAT GATAATTGCC CTGTGATAAC TAATCCTCTT CTTAATAATG	1860
GCTCGGGTGA AGTTCTGCTT CCCATCAGCG CTCCTCAAAA CTATTTAGTT TTCCAGCTCA	1920
AAGCCGAGGA TTCAGATGAA GGGCACAACT CCCAGCTGTT CTATACCATA CTGAGAGATC	1980
CAAGCAGATT GTTTGCCATT AACAAAGAAA GTGGTGAAGT GTTCCTGAAA AAACAATTAA	2040
ACTCTGACCA TTCAGAGGAC TTGAGCATAG TAGTTGCAGT GTATGACTTG GGAAGACCTT	2100
CATTATCCAC CAATGCTACA GTTAAATTCA TCCTCACCGA CTCTTTTCCT TCTAACGTTG	2160
AAGTCGTTAT TTTGCAACCA TCTGCAGAAG AGCAGCACCA GATCGATATG TCCATTATAT	2220
TCATTGCAGT GCTGGCTGGT GGTGTGCTT TGCTACTTTT GGCCATCTTT TTTGTGGCCT	2280
GTACTTGTA AAAGAAAGCT GGTGAATTTA AGCAGGTACC TGAACAACAT GGAACATGCA	2340

ATGAAGAACG CCTGTTAAGC ACCCCATCTC CCCAGTCGGT CTCTTCTTCT TTGTCTCAGT	2400
CTGAGTCATG CCAACTCTCC ATCAATACTG AATCTGAGAA TTGCAGCGTG TCCTCTAACC	2460
AAGAGCAGCA TCAGCAAACA GGCATAAAGC ACTCCATCTC TGTACCATCT TATCACACAT	2520
CTGGTTGGCA CCTGGACAAT TGTGCAATGA GCATAAGTGG ACATTCTCAC ATGGGGCACA	2580
TTAGTACAAA GGACAGTGGC AAAGGAGATA GTGACTTCAA TGACAGTGAC TCTGATACTA	2640
GTGGAGAATC ACAAAGAAG AGCATTGAGC AGCCAATGCA GGCACAAGCC AGTGCTCAAT	2700
ACACAGATGA ATCAGCAGGG TTCCGACATG CCGATAACTA TTCAGCCAC CGAATCAACA	2760
AGGGTCCAGA AAATGGGAAC TGCACATTGC AATATGAAAA GGGCTATAGA CTGTCTTACT	2820
CTGTAGCTCC TGCTCATTAC AATACCTACC ATGCAAGAAT GCCTAACCTG CACATACCGA	2880
ACCATACCCT TAGAGACCCT TATTACCATA TCAATAATCC TGTTGCTAAT CGGATGCACG	2940
CGGAATATGA AAGAGATTTA GTCAACAGAA GTGCAACGTT ATCTCCGCAG AGATCGTCTA	3000
GCAGATACCA AGAATTCAAT TACAGTCCGC AGATATCAAG ACAGCTTCAT CCTTCAGAAA	3060
TTGCTACAAC CTTTTAATCA TTAGGCATGC AAGTGAGAAT GCACAAAGGC AAGTGCTTTA	3120
GCATGAAAGC TAAATATATG GAGTCTCCCC TTTCCCTCTG ATGGATGGGG GGAGACACAG	3180
GACAGTGCAT AAATATACAG CTGCTTTCTA TTTGCATTTT ACTTGGAAT TTTTGTGTTT	3240
TTTTACATAT TTATTTTCC TGAATTGAAT GTGACATTGT CCTGTCACCT AACTAGCAAT	3300
TAAATCCACA GACCTACAGT CAAATATTTG AGGGCCCCTG AAACAGCACA TCAGTCAGGA	3360
CCTAAAGTGG CCTTTTTACT TTTAGCAGCT CCTGGGTCTG CCCTCTGTGT TAATCAGCCC	3420
CTGGTCAAGT CCTGAGTAGG ATCATGGCGT TTTTATATGC ATCTCACCTA CTTTGGACGT	3480
GATTTACACA TAATAGGAAA CGCTTGGTTT CAGTGAAGTC TGTGTTGTAT ATATTCTGTT	3540
ATATACACGC ATTTTGTGTT TGTGTATATA TTTCAAGTCC ATTCAGATAT GTGTATATAG	3600
TGCAGACCTT GTAAATTAAA TATTCTGATA CTTTTTCCTC AATAAATATT TAAAT	3655

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 323 amino acids
- (B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

Met Val Cys Cys Gly Pro Gly Arg Met Leu Leu Gly Trp Ala Gly Leu
1 5 10 15
Leu Val Leu Ala Ala Leu Cys Leu Leu Gln Val Pro Gly Ala Gln Ala
20 25 30
Ala Ala Cys Glu Pro Val Arg Ile Pro Leu Cys Lys Ser Leu Pro Trp
35 40 45
Asn Met Thr Lys Met Pro Asn His Leu His His Ser Thr Gln Ala Asn
50 55 60
Ala Ile Leu Ala Met Glu Gln Phe Glu Gly Leu Leu Gly Thr His Cys
65 70 75 80
Ser Pro Asp Leu Leu Phe Phe Leu Cys Ala Met Tyr Ala Pro Ile Cys
85 90 95
Thr Ile Asp Phe Gln His Glu Pro Ile Lys Pro Cys Lys Ser Val Cys
100 105 110
Glu Arg Ala Arg Gln Gly Cys Glu Pro Ile Leu Ile Lys Tyr Arg His
115 120 125
Ser Trp Pro Glu Ser Leu Ala Cys Asp Glu Leu Pro Val Tyr Asp Arg
130 135 140
Gly Val Cys Ile Ser Pro Glu Ala Ile Val Thr Ala Asp Gly Ala Asp
145 150 155 160
Phe Pro Met Asp Ser Ser Thr Gly His Cys Arg Gly Ala Ser Ser Glu
165 170 175
Arg Cys Lys Cys Lys Pro Val Arg Ala Thr Gln Lys Thr Tyr Phe Arg
180 185 190
Asn Asn Tyr Asn Tyr Val Ile Arg Ala Lys Val Lys Glu Val Lys Met
195 200 205
Lys Cys His Asp Val Thr Ala Val Val Glu Val Lys Glu Ile Leu Lys
210 215 220
Ala Ser Leu Val Asn Ile Pro Arg Asp Thr Val Asn Leu Tyr Thr Thr
225 230 235 240

Ser Gly Cys Leu Cys Pro Pro Leu Thr Val Asn Glu Glu Tyr Val Ile
245 250 255

Met Gly Tyr Glu Asp Glu Glu Arg Ser Arg Leu Leu Leu Val Glu Gly
260 265 270

Ser Ile Ala Glu Lys Trp Lys Asp Arg Leu Gly Lys Lys Val Lys Arg
275 280 285

Trp Asp Met Lys Leu Arg His Leu Gly Leu Gly Lys Thr Asp Ala Ser
290 295 300

Asp Ser Thr Gln Asn Gln Lys Ser Gly Arg Asn Ser Asn Pro Arg Pro
305 310 315 320

Ala Arg Ser

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2176 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

AAGCCTGGGA CCATGGTCTG CTGCGGCCCG GGACGGATGC TGCTAGGATG GGCCGGGTTG	60
CTAGTCCTGG CTGCTCTCTG CCTGCTCCAG GTGCCCCGAG CTCAGGCTGC AGCCTGTGAG	120
CCTGTCCGCA TCCCGCTGTG CAAGTCCCTT CCCTGGAACA TGACCAAGAT GCCCAACCAC	180
CTGCACCACA GCACCCAGGC TAACGCCATC CTGGCCATGG AACAGTTCGA AGGGCTGCTG	240
GGCACCCACT GCAGCCCGGA TCTTCTCTTC TTCCTCTGTG CAATGTACGC ACCCATTTGC	300
ACCATCGACT TCCAGCACGA GCCCATCAAG CCCTGCAAGT CTGTGTGTGA GCGCGCCCGA	360
CAGGGCTGCG AGCCCATTCT CATCAAGTAC CGCCACTCGT GGCCGGAAAG CTTGGCCTGC	420
GACGAGCTGC CGGTGTACGA CCGCGGCGTG TGCATCTCTC CTGAGGCCAT CGTCACCGCG	480
GACGGAGCGG ATTTTCCTAT GGATTCAAGT ACTGGACACT GCAGAGGGGC AAGCAGCGAA	540
CGTTGCAAAT GTAAGCCTGT CAGAGCTACA CAGAAGACCT ATTTCCGGAA CAATTACAAC	600

TTGTGTTGTT TAATGCTCCA TCAAGATGTC TAATAAAAGG AATATGGTTG TCAACAGAGA 2160
CGACAACAAC AACAAA 2176

(2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 325 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

Met	Val	Cys	Gly	Ser	Pro	Gly	Gly	Met	Leu	Leu	Leu	Arg	Ala	Gly	Leu	1	5	10	15
Leu	Ala	Leu	Ala	Ala	Leu	Cys	Leu	Leu	Arg	Val	Pro	Gly	Ala	Arg	Ala	20	25	30	
Ala	Ala	Cys	Glu	Pro	Val	Arg	Ile	Pro	Leu	Cys	Lys	Ser	Leu	Pro	Trp	35	40	45	
Asn	Met	Thr	Lys	Met	Pro	Asn	His	Leu	His	His	Ser	Thr	Gln	Ala	Asn	50	55	60	
Ala	Ile	Leu	Ala	Ile	Glu	Gln	Phe	Glu	Gly	Leu	Leu	Gly	Thr	His	Cys	65	70	75	80
Ser	Pro	Asp	Leu	Leu	Phe	Phe	Leu	Cys	Ala	Met	Tyr	Ala	Pro	Ile	Cys	85	90	95	
Thr	Ile	Asp	Phe	Gln	His	Glu	Pro	Ile	Lys	Pro	Cys	Lys	Ser	Val	Cys	100	105	110	
Glu	Arg	Ala	Arg	Gln	Gly	Cys	Glu	Pro	Ile	Leu	Ile	Lys	Tyr	Arg	His	115	120	125	
Ser	Trp	Pro	Glu	Asn	Leu	Ala	Cys	Glu	Glu	Leu	Pro	Val	Tyr	Asp	Arg	130	135	140	
Gly	Val	Cys	Ile	Ser	Pro	Glu	Ala	Ile	Val	Thr	Ala	Asp	Gly	Ala	Asp	145	150	155	160
Phe	Pro	Met	Asp	Ser	Ser	Asn	Gly	Asn	Cys	Arg	Gly	Ala	Ser	Ser	Glu	165	170	175	

Arg Cys Lys Cys Lys Pro Ile Arg Ala Thr Gln Lys Thr Tyr Phe Arg
 180 185 190
 Asn Asn Tyr Asn Tyr Val Ile Arg Ala Lys Val Lys Glu Ile Lys Thr
 195 200 205
 Lys Cys His Asp Val Thr Ala Val Val Glu Val Lys Glu Ile Leu Lys
 210 215 220
 Ser Ser Leu Val Asn Ile Pro Arg Asp Thr Val Asn Leu Tyr Thr Ser
 225 230 235 240
 Ser Gly Cys Leu Cys Pro Pro Leu Asn Val Asn Glu Glu Tyr Ile Ile
 245 250 255
 Met Gly Tyr Glu Asp Glu Glu Arg Ser Arg Leu Leu Leu Val Glu Gly
 260 265 270
 Ser Ile Ala Glu Lys Trp Lys Asp Arg Leu Gly Lys Lys Val Lys Arg
 275 280 285
 Trp Asp Met Lys Leu Arg His Leu Gly Leu Ser Lys Ser Asp Ser Ser
 290 295 300
 Asn Ser Asp Ser Thr Gln Ser Gln Lys Ser Gly Arg Asn Ser Asn Pro
 305 310 315 320
 Arg Gln Ala Arg Asn
 325

(2) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1893 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

GGCGGAGCGG GCCTTTTGGC GTCCACTGCG CGGCTGCACC CTGCCCCATC TGCCGGGATC 60
 ATGGTCTGCG GCAGCCCGGG AGGGATGCTG CTGCTGCGGG CCGGGCTGCT TGCCCTGGCT 120
 GCTCTCTGCC TGCTCCGGGT GCCCGGGGCT CGGGCTGCAG CCTGTGAGCC CGTCCGCATC 180
 CCCCTGTGCA AGTCCCTGCC CTGGAACATG ACTAAGATGC CCAACCACCT GCACCACAGC 240

ACTCAGGCCA	ACGCCATCCT	GGCCATCGAG	CAGTTCGAAG	GTCTGCTGGG	CACCCACTGC	300
AGCCCCGATC	TGCTCTTCTT	CCTCTGTGCC	ATGTACGCGC	CCATCTGCAC	CATTGACTTC	360
CAGCACGAGC	CCATCAAGCC	CTGTAAGTCT	GTGTGCGAGC	GGGCCCCGCA	GGGCTGTGAG	420
CCCATACTCA	TCAAGTACCG	CCACTCGTGG	CCGGAGAACC	TGGCCTGCGA	GGAGCTGCCA	480
GTGTACGACA	GGGGCGTGTG	CATCTCTCCC	GAGGCCATCG	TTACTGCGGA	CGGAGCTGAT	540
TTTCCTATGG	ATTCTAGTAA	CGGAACTGT	AGAGGGGCAA	GCAGTGAACG	CTGTAAATGT	600
AAGCCTATTA	GAGCTACACA	GAAGACCTAT	TTCCGGAACA	ATTACAATA	TGTCATTCCG	660
GCTAAAGTTA	AAGAGATAAA	GAATAAGTGC	CATGATGTGA	CTGCAGTAGT	GGAGGTGAAG	720
GAGATTCTAA	AGTCCTCTCT	GGTAAACATT	CCACGGGACA	CTGTCAACCT	CTATACCAGC	780
TCTGGCTGCC	TCTGCCCTCC	ACTTAATGTT	AATGAGGAAT	ATATCATCAT	GGGCTATGAA	840
GATGAGGAAC	GTTCCAGATT	ACTCTTGGTG	GAAGGCTCTA	TAGCTGAGAA	GTGGAAGGAT	900
CGACTCGGTA	AAAAAGTTAA	GCGCTGGGAT	ATGAAGCTTC	GTCATCTTGG	ACTCAGTAAA	960
AGTGATTCTA	GCAATAGTGA	TTCCACTCAG	AGTCAGAAGT	CTGGCAGGAA	CTCGAACCCC	1020
CGGCAAGCAC	GCAACTAAAT	CCCGAAATAC	AAAAAGTAAC	ACAGTGGACT	TCCTATTAAG	1080
ACTTACTTGC	ATTGCTGGAC	TAGCAAAGGA	AAATTGCACT	ATTGCACATC	ATATTCTATT	1140
GTTTACTATA	AAAATCATGT	GATAACTGAT	TATTACTTCT	GTTTCTCTTT	TGGTTTCTGC	1200
TTCTCTCTTC	TCTCAACCCC	TTTGTAATGG	TTTGGGGGCA	GACTCTTAAG	TATATTGTGA	1260
GTTTTCTATT	TCACTAATCA	TGAGAAAAAC	TGTTCTTTTG	CAATAATAAT	AAATTAAACA	1320
TGCTGTTACC	AGAGCCTCTT	TGCTGAGTCT	CCAGATGTTA	ATTTACTTTC	TGCACCCCAA	1380
TTGGGAATGC	AATATTGGAT	GAAAAGAGAG	GTTTCTGGTA	TTACACAGAA	GCTAGATATG	1440
CCTTAAACA	TACTCTGCCG	ATCTAATTAC	AGCCTTATTT	TTGTATGCCT	TTTGGGCATT	1500
CTCCTCATGC	TTAGAAAGTT	CCAAATGTTT	ATAAAGGTAA	AATGGCAGTT	TGAAGTCAAA	1560
TGTCACATAG	GCAAAGCAAT	CAAGCACCAG	GAAGTGTTTA	TGAGGAAACA	ACACCCAAGA	1620
TGAATTATTT	TTGAGACTGT	CAGGAAGTAA	AATAAATAGG	AGCTTAAGAA	AGAACATTTT	1680
GCCTGATTGA	GAAGCACAAC	TGAAACCAGT	AGCCGCTGGG	GTGTTAATGG	TAGCATTCTT	1740
CTTTTGGCAA	TACATTTGAT	TTGTTCATGA	ATATATTAAT	CAGCATTAGA	GAAATGAATT	1800

